



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/911,048A  
Source: 1600  
Date Processed by STIC: 11/4/2003

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221**

**Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/911, 048A
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO: X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFW16

## RAW SEQUENCE LISTING

DATE: 11/04/2003

PATENT APPLICATION: US/09/911,048A

TIME: 09:54:39

Input Set : A:\DAM552-00.SequenceListing.txt

Output Set: N:\CRF4\11032003\I911048A.raw

3 <110> APPLICANT: Davis, Julian E.  
 4       Kao, Richard  
 5       Young, Ronald  
 8 <120> TITLE OF INVENTION: METHODS FOR DETECTING RIBOSOME INACTIVATING PROTEINS  
 10 <130> FILE REFERENCE: DAM 552-00  
 12 <140> CURRENT APPLICATION NUMBER: 09/911,048A  
 13 <141> CURRENT FILING DATE: 2001-07-23  
 15 <150> PRIOR APPLICATION NUMBER: 60/222,002  
 16 <151> PRIOR FILING DATE: 2000-07-31  
 18 <160> NUMBER OF SEQ ID NOS: 1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 19  
 22 <212> TYPE: RNA  
 23 <213> ORGANISM: Artificial Sequence  
 W--> 24 <220> FEATURE:  
 W--> 26 <221> NAME/KEY: miscellaneous feature  
 27 <222> LOCATION: 12  
 28 <223> OTHER INFORMATION: n=adenine, adenine analog, adenine derivative  
 30 <400> SEQUENCE: 1  
 W--> 31 uuuuucgcgc gngagcgcg                      19

Does Not Comply  
Corrected Disclosure Needed

needs explanation in 2207-2237

section  
(see  
item 11 on  
Error  
summary  
sheet)

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 11/04/2003  
PATENT APPLICATION: US/09/911,048A      TIME: 09:54:40

Input Set : A:\DAM552-00.SequenceListing.txt  
Output Set: N:\CRF4\11032003\I911048A.raw

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 12

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/911,048A

DATE: 11/04/2003

TIME: 09:54:40

Input Set : A:\DAM552-00.SequenceListing.txt

Output Set: N:\CRF4\11032003\I911048A.raw

L:24 M:283 W: Missing Blank Line separator, <220> field identifier

L:26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1

L:31 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0